We claim:

1. A method of identifying a compound that modulates insulin receptor activity, comprising producing a compound that interacts with all or part of the fitted quaternary structure of insulin receptor or a fragment or derivative thereof and which thereby modulates insulin receptor activity.
2. The method of claim 1, further comprising synthesizing the compound.
3. A method of identifying a compound that modulates insulin receptor activity, comprising comparing the structure of a compound for modulating insulin receptor activity to all or part of the fitted quaternary structure of insulin receptor or a fragment or derivative thereof to determine whether the compound is likely to modulate insulin receptor activity.
4. The method of claim 1 or 3, further comprising determining whether the compound modulates the activity of the insulin receptor or a fragment or a derivative thereof having insulin receptor activity in an *in vivo* or *in vitro* assay.
5. The method of claim 1 or 3, wherein the compound comprises an insulin receptor agonist or an IR antagonist.
6. The method of claim 1 or 3, wherein the fitted quaternary structure of insulin receptor comprises substantially the entire fitted quaternary structure of insulin receptor.
7. The method of claim 1 or 3, further comprising:

a) introducing into a computer program information defining a ligand binding site conformation including at least one residue from monomer A in Table I and at least one residue from monomer B in Table I, the ligand binding site defined by the approximate amino acid distances listed in Table I, wherein the program displays the quaternary structure thereof;

b) comparing the structural coordinates of the compound to the structural coordinates of the ligand binding site and determining whether the

compound fits spatially into the ligand binding site and is capable of changing insulin receptor from an inactive conformation to an active conformation or biasing insulin receptor toward an active conformation;

wherein the ability to change insulin receptor from an inactive conformation to an active conformation or bias insulin receptor toward an active conformation is predictive of the ability of the compound to agonize insulin receptor activity.

8. The method of claim 7, further comprising preparing the compound that fits spatially into the ligand binding site and determining whether the compound agonizes insulin receptor activity in an insulin receptor activity assay.

9. The method of claim 1 or 3, further comprising:

a) introducing into a computer program information defining a ligand binding site conformation including at least one residue from monomer A in Table I and at least one residue from monomer B in Table 1, the ligand binding site defined by the approximate amino acid coordinates listed in Table 1, wherein the program displays the quaternary structure thereof;

b) comparing the structural coordinates of the compound to the structural coordinates of the ligand binding site and determining whether the compound fits spatially into the ligand binding site and is capable of changing insulin receptor from an active conformation to an inactive conformation or biasing insulin receptor toward an inactive conformation;

wherein the ability to change insulin receptor from an active conformation to an inactive conformation or bias insulin receptor toward an inactive conformation is predictive of the ability of the compound to antagonize insulin receptor activity.

10. The method of claim 9, further comprising preparing the compound that fits spatially into the ligand binding site and determining whether the test compound antagonizes insulin receptor activity in an insulin receptor activity assay.

11. The method of claim 1 or 3, further comprising:

a) introducing into a computer program information defining a cam including at least one residue from the Cam-loop segment in Table 2 and at least one residue from the L1 surface in Table 2, wherein the program displays the quaternary structure thereof;

b) comparing the structural coordinates of the compound to the structural coordinates of the cam and determining whether the compound interacts with the cam and is capable of changing insulin receptor from an inactive conformation to an active conformation or biasing insulin receptor toward an active conformation;

wherein the ability to change insulin receptor from an inactive conformation to an active conformation is predictive of the ability of the compound to agonize insulin receptor activity.

12. The method of claim 11, further comprising preparing the compound that interacts with the cam and determining whether the test compound agonizes insulin receptor activity in an insulin receptor activity assay.

13. The method of claim 1 or 3, further comprising:

a) introducing into a computer program information defining a cam conformation including at least one residue from the Cam-loop segment in Table 2 and at least one residue from the L1 surface in Table 2, wherein the program displays the quaternary structure thereof;

b) comparing the structural coordinates of the compound to the structural coordinates of the cam and determining whether the compound interacts with the cam and is capable of changing insulin receptor from an active conformation to an inactive conformation;

wherein the ability to change insulin receptor from an active conformation to an inactive conformation or bias insulin receptor toward an inactive conformation is predictive of the ability of the compound to antagonize insulin receptor activity.

14. The method of claim 13, further comprising preparing the compound that interacts with the cam and determining whether the test compound

antagonizes insulin receptor activity in an insulin receptor activity assay.

15. The method of any of claims 1 or 3, wherein the insulin receptor is bound to insulin.

16. A computer medium having recorded thereon data of an insulin receptor, said data sufficient to model all or part of the fitted quaternary structure of the receptor.

17. The computer medium of claim 16, wherein the data comprises structural coordinates of an IR receptor, the coordinates sufficient to model all or part of the quaternary structure of the receptor.

18. The computer medium of claim 16, wherein the quaternary structure of the receptor comprises substantially all of the quaternary structure of the receptor.